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1/21

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SEQUENCE LISTING

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<110> OncoMab GmbH et al.

<120> Neoplasm-Specific Polypeptides and Their
Uses

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<151> 2004-01-26

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 Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
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 Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
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    aaa gtc agt tat tca ttg gcc aaa tcc tgt aaa agt gac ttg aag aaa    720
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Ile Gln Thr Ala Cys Lys His Ile Arg Ser Gly Asp Pro Met Ile Leu	
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3114

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 Ser Asp Asp Phe His Leu Asp Arg His Leu Tyr Phe Ala Cys Arg Asp
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Thr	Val	Arg	Asn	Asp	Thr	Leu	Gln	Glu	Ala	Lys	Glu	His	Arg	Val	Ser
			645						650					655	
Leu	Lys	Cys	Arg	Arg	Gln	Leu	Arg	Val	Glu	Glu	Leu	Glu	Met	Thr	Glu
		660						665					670		
Asp	Ile	Arg	Leu	Glu	Pro	Asp	Leu	Tyr	Glu	Ala	Cys	Lys	Ser	Asp	Ile
	675						680					685			
Lys	Asn	Phe	Cys	Ser	Ala	Val	Gln	Tyr	Gly	Asn	Ala	Gln	Ile	Ile	Glu
	690					695					700				
Cys	Leu	Lys	Glu	Asn	Lys	Lys	Gln	Leu	Ser	Thr	Arg	Cys	His	Gln	Lys
705					710					715					720
Val	Phe	Lys	Leu	Gln	Glu	Thr	Glu	Met	Met	Asp	Pro	Glu	Leu	Asp	Tyr
			725						730					735	
Thr	Leu	Met	Arg	Val	Cys	Lys	Gln	Met	Ile	Lys	Lys	Phe	Cys	Pro	Glu
		740						745					750		
Ala	Asp	Ser	Lys	Thr	Met	Leu	Gln	Cys	Leu	Lys	Gln	Asn	Lys	Asn	Ser
	755						760					765			
Glu	Leu	Met	Asp	Pro	Lys	Cys	Lys	Gln	Met	Ile	Thr	Lys	Arg	Gln	Ile
	770					775					780				
Thr	Gln	Asn	Thr	Asp	Tyr	Arg	Leu	Asn	Pro	Met	Leu	Arg	Lys	Ala	Cys
785					790					795					800
Lys	Ala	Asp	Ile	Pro	Lys	Phe	Cys	His	Gly	Ile	Leu	Thr	Lys	Ala	Lys

				805				810				815				
Asp	Asp	Ser	Glu	Leu	Glu	Gly	Gln	Val	Ile	Ser	Cys	Leu	Lys	Leu	Arg	
820				825				830								
Tyr	Ala	Asp	Gln	Arg	Leu	Ser	Ser	Asp	Cys	Glu	Asp	Gln	Ile	Arg	Ile	
835				840				845								
Ile	Ile	Gln	Glu	Ser	Ala	Leu	Asp	Tyr	Arg	Leu	Asp	Pro	Gln	Leu	Gln	
850				855				860								
Leu	His	Cys	Ser	Asp	Glu	Ile	Ser	Ser	Leu	Cys	Ala	Glu	Glu	Ala	Ala	
865					870				875				880			
Ala	Gln	Glu	Gln	Thr	Gly	Gln	Val	Glu	Glu	Cys	Leu	Lys	Val	Asn	Leu	
885				890				895								
Leu	Lys	Ile	Lys	Thr	Glu	Leu	Cys	Lys	Lys	Glu	Val	Leu	Asn	Met	Leu	
900				905				910								
Lys	Glu	Ser	Lys	Ala	Asp	Ile	Phe	Val	Asp	Pro	Val	Leu	His	Thr	Ala	
915				920				925								
Cys	Ala	Leu	Asp	Ile	Lys	His	His	Cys	Ala	Ala	Ile	Thr	Pro	Gly	Arg	
930				935				940								
Gly	Arg	Gln	Met	Ser	Cys	Leu	Met	Glu	Ala	Leu	Glu	Asp	Lys	Arg	Val	
945					950				955				960			
Arg	Leu	Gln	Pro	Glu	Cys	Lys	Lys	Arg	Leu	Asn	Asp	Arg	Ile	Glu	Met	
965				970				975								
Trp	Ser	Tyr	Ala	Ala	Lys	Val	Ala	Pro	Ala	Asp	Gly	Phe	Ser	Asp	Leu	
980				985				990								
Ala	Met	Gln	Val	Met	Thr	Ser	Pro	Ser	Lys	Asn	Tyr	Ile	Leu	Ser	Val	
995				1000				1005								
Ile	Ser	Gly	Ser	Ile	Cys	Ile	Leu	Phe	Leu	Ile	Gly	Leu	Met	Cys	Gly	
1010				1015				1020								
Arg	Ile	Thr	Lys	Arg	Val	Thr	Arg	Glu	Leu	Lys	Asp	Arg				
1025					1030				1035							

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<210> 7
<211> 1177
<212> PRT
<213> Homo sapiens
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<400> 7
Met Ala Ala Cys Gly Arg Val Arg Arg Met Phe Arg Leu Ser Ala Ala
 1          5          10          15
Leu His Leu Leu Leu Leu Phe Ala Ala Gly Gly Arg Asn Ser Pro Ala
          20          25          30
Arg Ala Ser His Ser Gln Gly Gln Gly Pro Gly Ala Asn Phe Val Ser
          35          40          45
Phe Val Gly Gln Ala Gly Gly Gly Gly Pro Ala Gly Gln Gln Leu Pro
          50          55          60
Gln Leu Pro Gln Ser Ser Gln Leu Gln Gln Gln Gln Gln Gln Gln
65          70          75          80
Gln Gln Gln Gln Pro Gln Pro Pro Gln Pro Pro Phe Pro Ala Gly Gly
          85          90          95
Pro Pro Arg Arg Gly Gly Ala Gly Ala Gly Gly Gly Trp Lys Leu Ala
          100          105          110
Glu Glu Glu Ser Cys Arg Glu Asp Val Thr Arg Val Cys Pro Lys His
          115          120          125
Thr Trp Ser Asn Asn Leu Ala Val Leu Glu Cys Leu Gln Asp Val Arg
          130          135          140
Glu Pro Glu Asn Glu Ile Ser Ser Asp Cys Asn His Leu Leu Trp Asn
145          150          155          160

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Tyr	Lys	Leu	Asn	Leu	Thr	Thr	Asp	Pro	Lys	Phe	Glu	Ser	Val	Ala	Arg
				165					170					175	
Glu	Val	Cys	Lys	Ser	Thr	Ile	Thr	Glu	Ile	Lys	Glu	Cys	Ala	Asp	Glu
			180					185					190		
Pro	Val	Gly	Lys	Gly	Tyr	Met	Val	Ser	Cys	Leu	Val	Asp	His	Arg	Gly
		195					200					205			
Asn	Ile	Thr	Glu	Tyr	Gln	Cys	His	Gln	Tyr	Ile	Thr	Lys	Met	Thr	Ala
	210					215					220				
Ile	Ile	Phe	Ser	Asp	Tyr	Arg	Leu	Ile	Cys	Gly	Phe	Met	Asp	Asp	Cys
225					230					235					240
Lys	Asn	Asp	Ile	Asn	Ile	Leu	Lys	Cys	Gly	Ser	Ile	Arg	Leu	Gly	Glu
				245					250					255	
Lys	Asp	Ala	His	Ser	Gln	Gly	Glu	Val	Val	Ser	Cys	Leu	Glu	Lys	Gly
			260					265					270		
Leu	Val	Lys	Glu	Ala	Glu	Glu	Arg	Glu	Pro	Lys	Ile	Gln	Val	Ser	Glu
		275					280					285			
Leu	Cys	Lys	Lys	Ala	Ile	Leu	Arg	Val	Ala	Glu	Leu	Ser	Ser	Asp	Asp
	290					295					300				
Phe	His	Leu	Asp	Arg	His	Leu	Tyr	Phe	Ala	Cys	Arg	Asp	Asp	Arg	Glu
305					310					315					320
Arg	Phe	Cys	Glu	Asn	Thr	Gln	Ala	Cys	Glu	Gly	Arg	Val	Tyr	Lys	Cys
				325					330					335	
Leu	Phe	Asn	His	Lys	Phe	Glu	Glu	Ser	Met	Ser	Glu	Lys	Cys	Arg	Glu
			340					345					350		
Ala	Leu	Thr	Thr	Arg	Gln	Lys	Leu	Ile	Ala	Gln	Asp	Tyr	Lys	Val	Ser
		355					360					365			
Tyr	Ser	Leu	Ala	Lys	Ser	Cys	Lys	Ser	Asp	Leu	Lys	Lys	Tyr	Arg	Cys
	370					375					380				
Asn	Val	Glu	Asn	Leu	Pro	Arg	Ser	Arg	Glu	Ala	Arg	Leu	Ser	Tyr	Leu
385					390					395					400
Leu	Met	Cys	Leu	Glu	Ser	Ala	Val	His	Arg	Gly	Arg	Gln	Val	Ser	Ser
				405					410					415	
Glu	Cys	Gln	Gly	Glu	Met	Leu	Asp	Tyr	Arg	Arg	Met	Leu	Met	Glu	Asp
			420					425				430			
Phe	Ser	Leu	Ser	Pro	Glu	Ile	Ile	Leu	Ser	Cys	Arg	Gly	Glu	Ile	Glu
		435				440						445			
His	His	Cys	Ser	Gly	Leu	His	Arg	Lys	Gly	Arg	Thr	Leu	His	Cys	Leu
	450					455					460				
Met	Lys	Val	Val	Arg	Gly	Glu	Lys	Cys	Asn	Leu	Gly	Met	Asn	Cys	Gln
465					470				475						480
Gln	Ala	Leu	Gln	Thr	Leu	Ile	Gln	Glu	Thr	Asp	Pro	Gly	Ala	Asp	Tyr
				485					490					495	
Arg	Ile	Asp	Arg	Ala	Leu	Asn	Glu	Ala	Cys	Glu	Ser	Val	Ile	Gln	Thr
			500					505					510		
Ala	Cys	Lys	His	Ile	Arg	Ser	Gly	Asp	Pro	Met	Ile	Ser	Ser	Cys	Leu
		515					520					525			
Met	Glu	His	Leu	Tyr	Thr	Glu	Lys	Met	Val	Glu	Asp	Cys	Glu	His	Arg
	530					535					540				
Leu	Leu	Glu	Leu	Gln	Tyr	Phe	Ile	Ser	Arg	Asp	Trp	Lys	Leu	Asp	Pro
545					550					555					560
Val	Leu	Tyr	Arg	Lys	Cys	Gln	Gly	Asp	Ala	Ser	Arg	Leu	Cys	His	Thr
				565					570					575	
His	Gly	Trp	Asn	Glu	Thr	Ser	Glu	Phe	Met	Pro	Gln	Gly	Ala	Val	Phe
			580					585					590		
Ser	Cys	Leu	Tyr	Arg	Glu	Ala	Tyr	Arg	Thr	Glu	Glu	Gln	Gly	Arg	Arg
		595					600					605			
Leu	Ser	Arg	Glu	Cys	Arg	Ala	Glu	Val	Gln	Arg	Ile	Leu	His	Gln	Arg

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610	615	620
Ala Met Asp Val Lys Leu Asp Pro Ala Leu Gln Asp Lys Cys Leu Ile		
625	630	635
Asp Leu Gly Lys Trp Cys Ser Glu Lys Thr Glu Thr Gly Gln Glu Leu		640
	645	650
Glu Cys Leu Gln Asp His Leu Asp Asp Leu Val Val Glu Cys Arg Asp		655
	660	665
Ile Val Gly Asn Leu Thr Glu Leu Glu Ser Glu Asp Ile Gln Ile Glu		670
	675	680
Ala Leu Leu Met Arg Ala Cys Glu Pro Ile Ile Gln Thr Phe Cys His		685
	690	695
Asp Ala Asp Asn Gln Ile Asp Ser Gly Asp Leu Met Glu Cys Leu Ile		700
705	710	715
Gln Asn Lys His Gln Lys Asp Met Asn Glu Lys Cys Ala Ile Gly Val		720
	725	730
Thr His Phe Gln Leu Val Gln Met Lys Asp Phe Arg Phe Ser Tyr Lys		735
	740	745
Phe Lys Met Ala Cys Lys Glu Asp Val Leu Lys Leu Cys Pro Asn Ile		750
	755	760
Lys Lys Lys Val Asp Val Val Ile Cys Leu Ser Thr Thr Val Arg Asn		765
	770	775
Asp Thr Leu Gln Glu Ala Lys Glu His Arg Val Ser Leu Lys Cys Arg		780
785	790	795
Arg Gln Leu Arg Val Glu Glu Leu Glu Met Thr Glu Asp Ile Arg Leu		800
	805	810
Glu Pro Asp Leu Tyr Glu Ala Cys Lys Ser Asp Ile Lys Asn Phe Cys		815
	820	825
Ser Ala Val Gln Tyr Gly Asn Ala Gln Ile Ile Glu Cys Leu Lys Glu		830
	835	840
Asn Lys Lys Gln Leu Ser Thr Arg Cys His Gln Lys Val Phe Lys Leu		845
	850	855
Gln Glu Thr Glu Met Met Asp Pro Glu Leu Asp Tyr Thr Leu Met Arg		860
865	870	875
Val Cys Lys Gln Met Ile Lys Arg Phe Cys Pro Glu Ala Asp Ser Lys		880
	885	890
Thr Met Leu Gln Cys Leu Lys Gln Asn Lys Asn Ser Glu Leu Met Asp		895
	900	905
Pro Lys Cys Lys Gln Met Ile Thr Lys Arg Gln Ile Thr Gln Asn Thr		910
	915	920
Asp Tyr Arg Leu Asn Pro Met Leu Arg Lys Ala Cys Lys Ala Asp Ile		925
	930	935
Pro Lys Phe Cys His Gly Ile Leu Thr Lys Ala Lys Asp Asp Ser Glu		940
945	950	955
Leu Glu Gly Gln Val Ile Ser Cys Leu Lys Leu Arg Tyr Ala Asp Gln		960
	965	970
Arg Leu Ser Ser Asp Cys Glu Asp Gln Ile Arg Ile Ile Ile Gln Glu		975
	980	985
Ser Ala Leu Asp Tyr Arg Leu Asp Pro Gln Leu Gln Leu His Cys Ser		990
	995	1000
Asp Glu Ile Ser Ser Leu Cys Ala Glu Glu Ala Ala Gln Glu Gln		1005
	1010	1015
Thr Gly Gln Val Glu Glu Cys Leu Lys Val Asn Leu Leu Lys Ile Lys		1020
1025	1030	1035
Thr Glu Leu Cys Lys Lys Glu Val Leu Asn Met Leu Lys Glu Ser Lys		1040
	1045	1050
Ala Asp Ile Phe Val Asp Pro Val Leu His Thr Ala Cys Ala Leu Asp		1055
	1060	1065
		1070

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Ile Lys His His Cys Ala Ala Leu Thr Pro Gly Arg Gly Arg Gln Met
  1075                      1080                      1085
Ser Cys Leu Met Glu Ala Leu Glu Asp Lys Arg Val Arg Leu Gln Pro
  1090                      1095                      1100
Glu Cys Lys Lys Arg Leu Asn Asp Arg Ile Glu Met Trp Ser Tyr Ala
  1105                      1110                      1115                      1120
Ala Lys Val Ala Pro Ala Asp Gly Phe Ser Asp Leu Ala Met Gln Val
                      1125                      1130                      1135
Met Thr Ser Pro Ser Lys Asn Tyr Ile Leu Ser Val Ile Ser Gly Ser
                      1140                      1145                      1150
Ile Cys Ile Leu Phe Leu Ile Gly Leu Met Cys Gly Arg Ile Thr Lys
                      1155                      1160                      1165
Arg Val Thr Arg Glu Leu Lys Asp Arg
  1170                      1175

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<210> 8
<211> 1179
<212> PRT
<213> Homo sapiens

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<400> 8
Met Ala Ala Cys Gly Arg Val Arg Arg Met Phe Arg Leu Ser Ala Ala
  1          5          10          15
Leu His Leu Leu Leu Leu Phe Ala Ala Gly Ala Glu Lys Leu Pro Gly
          20          25          30
His Gly Val His Ser Gln Gly Gln Gly Pro Gly Ala Asn Phe Val Ser
          35          40          45
Phe Val Gly Gln Ala Gly Gly Gly Gly Pro Ala Gly Gln Gln Leu Pro
          50          55          60
Gln Leu Leu Gln Ser Ser Gln Leu Gln Gln Gln Gln Gln Gln Gln
  65          70          75          80
Gln Gln Gln Gln Leu Gln Pro Pro Gln Pro Pro Phe Pro Ala Gly Gly
          85          90          95
Pro Pro Ala Arg Arg Gly Gly Ala Gly Ala Gly Gly Gly Trp Lys Leu
          100          105          110
Ala Glu Glu Glu Ser Cys Arg Glu Asp Val Thr Arg Val Cys Pro Lys
          115          120          125
His Thr Trp Ser Asn Asn Leu Ala Val Leu Glu Cys Leu Gln Asp Val
          130          135          140
Arg Glu Pro Glu Asn Glu Ile Ser Ser Asp Cys Asn His Leu Leu Trp
  145          150          155          160
Asn Tyr Lys Leu Asn Leu Thr Thr Asp Pro Lys Phe Glu Ser Val Ala
          165          170          175
Arg Glu Val Cys Lys Ser Thr Ile Thr Glu Ile Lys Glu Cys Ala Asp
          180          185          190
Glu Pro Val Gly Lys Gly Tyr Met Val Ser Cys Leu Val Asp His Arg
          195          200          205
Gly Asn Ile Thr Glu Tyr Gln Cys His Gln Tyr Ile Thr Lys Met Thr
          210          215          220
Ala Ile Ile Phe Ser Asp Tyr Arg Leu Ile Cys Gly Phe Met Asp Asp
  225          230          235          240
Cys Lys Asn Asp Ile Asn Ile Leu Lys Cys Gly Ser Ile Arg Leu Gly
          245          250          255
Glu Lys Asp Ala His Ser Gln Gly Glu Val Val Ser Cys Leu Glu Lys
          260          265          270
Gly Leu Val Lys Glu Ala Glu Glu Arg Glu Pro Lys Ile Gln Val Ser

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<210> 9
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 9
gcttggagaa aggcctggtg aa 22

<210> 10
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 10
tggcacttgc ggtacaggac ag 22

<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 11
gcagcttcag cagcaacagc a 21

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 12
cagctcagcc acccgagaa tg 22

<210> 13
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 13
gcttggagaa aggcctggtg aa 22

<210> 14

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 14
tggcacttgc ggtacaggac ag

22

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 15
gaacaccgtc tcttagagct gc

22

<210> 16
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 16
gcttcctgca gagtgtcatt gc

22

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 17
ggaggacgtg ttgaagcttt gc

22

<210> 18
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
ccagggcaca agcagtatga ag

22

<210> 19
<211> 22
<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 19

caacagcaga caggtcaggt gg

22

<210> 20

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 20

ccggaagttc tgttggtatg ag

22

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 21

atttaaccct cactaaaggg

20

<210> 22

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 22

gtaatacgac tcactatagg gc

22

<210> 23

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 23

ccggaagttc tgttggtatg ag

22

<210> 24

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 24

gtggaaggac tcatgaccac agtc

24

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 25

catgtgggcc atgaggtcca ccac

24

<210> 26

<211> 312

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

 $\langle 222 \rangle \quad (1) \dots (312)$

<223>

<400> 26

agg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc 48
Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
1 5 10 15

tat ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg 96
Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
20 25 30

gtg gca gtt ata tca tat gat gga agt aat aaa tac tat gca gac tcc 144
Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser
35 40 45

gtg aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg 192
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
50 55 60

tat	ctg	caa	atg	aac	agc	ctg	aga	gct	gag	gac	acg	gct	gtg	tat	tac	240
Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	
65					70					75					80	

tgt	gcg	agg	tcg	act	acg	agg	tct	tat	cct	cta	tac	ggc	atg	gac	gtt	288
Cys	Ala	Arg	Ser	Thr	Thr	Arg	Ser	Tyr	Pro	Leu	Tyr	Gly	Met	Asp	Val	
				85					90					95		

tgg ggc caa ggg aac cct gtc acc 312
Trp Gly Gln Gly Asn Pro Val Thr
100

<210> 27
 <211> 399
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(399)
 <223>

<400> 27
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 Val Thr Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro
 1 5 10 15
 gga cag acg gcc agt att acc tgt ggg gga aat aac att gga agt aaa 96
 Gly Gln Thr Ala Ser Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys
 20 25 30
 agt gtg cac tgg tac cat cag aag cca ggc cag gcc cct gtg ctg gtc 144
 Ser Val His Trp Tyr His Gln Lys Pro Gly Gln Ala Pro Val Leu Val
 35 40 45
 gtc tat gat gat agc gac cgg ccc tca ggg atc cct gag cga ttc tct 192
 Val Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser
 50 55 60
 ggc tcc aac tct ggg aac acg gcc acc ctg acc atc acc agg gtc gaa 240
 Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Thr Arg Val Glu
 65 70 75 80
 gcc ggg gat gag gcc gac tat tac tgt cag gtg tgg gat agt agt agt 288
 Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser
 85 90 95
 gat ctc aat tgg gtg ttc ggc gga agg acc caa gct gac cgt cct acg 336
 Asp Leu Asn Trp Val Phe Gly Gly Arg Thr Gln Ala Asp Arg Pro Thr
 100 105 110
 tca gcc caa ggc tgc ccc tcc ggt cac tct gtt ccc cgc ccc cct ctg 384
 Ser Ala Gln Gly Cys Pro Ser Gly His Ser Val Pro Arg Pro Pro Leu
 115 120 125
 aag agc ttc aag ctt 399
 Lys Ser Phe Lys Leu
 130

<210> 28
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 28
 Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
 1 5 10 15
 Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp

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      20      25      30
Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser
      35      40      45
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
      50      55      60
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
      65      70      75      80
Cys Ala Arg Ser Thr Thr Arg Ser Tyr Pro Leu Tyr Gly Met Asp Val
      85      90      95
Trp Gly Gln Gly Asn Pro Val Thr
      100

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<210> 29
 <211> 133
 <212> PRT
 <213> Homo sapiens

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<400> 29
Val Thr Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro
  1      5      10      15
Gly Gln Thr Ala Ser Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys
      20      25      30
Ser Val His Trp Tyr His Gln Lys Pro Gly Gln Ala Pro Val Leu Val
      35      40      45
Val Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser
      50      55      60
Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Thr Arg Val Glu
      65      70      75      80
Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser
      85      90      95
Asp Leu Asn Trp Val Phe Gly Gly Arg Thr Gln Ala Asp Arg Pro Thr
      100      105      110
Ser Ala Gln Gly Cys Pro Ser Gly His Ser Val Pro Arg Pro Pro Leu
      115      120      125
Lys Ser Phe Lys Leu
      130

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<210> 30
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 30
 caagagcaga caggtcaggt gg

22